OM protein - protein search, using sw model

Run on:                March 17, 2006, 17:50:39 ; Search time 193 Seconds
                       (without alignments)
                       2160.469 Million cell updates/sec

Title:                 US-10-667-281-2
Perfect score:         5183
Sequence:              1 GNAERAPGSRSFGPVPTLLL.........CDPLKKPKHFIDFCTWAECS 949

Scoring table:         BLOSUM62
                       Gapop 10.0 , Gapext 0.5

Searched:              2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:    2443163

Post-processing:       Minimum Match 0%
                       Listing first 10 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :             A_Geneseq_21:*
                       Maximum Match 100%
                       Listing first 10 summaries

                       1: geneseqp19980s:*
                       2: geneseqp1990s:*
                       3: geneseqp2000s:*
                       4: geneseqp2001s:*
                       5: geneseqp2002s:*
                       6: geneseqp2003aa:*
                       7: geneseqp2003bs:*
                       8: geneseqp2004s:*
                       9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5183 | 100.0 | 949 | 7 | ADG72483 | Adg72483 Human agg |
| 2 | 5183 | 100.0 | 949 | 9 | ADZ21014 | Adz21014 Human agg |
| 3 | 5183 | 100.0 | 950 | 9 | ADZ21015 | Adz21015 Human agg |
| 4 | 5174 | 99.8 | 950 | 8 | ADG20218 | Adg20218 Human PRO |
| 5 | 5174 | 99.8 | 950 | 8 | ADG39942 | Adg39942 Human myo |
| 6 | 5174 | 99.8 | 950 | 9 | AEC01581 | Aec01581 Human ADA |
| 7 | 5174 | 99.8 | 967 | 8 | ADG39940 | Adg39940 Human myo |
| 8 | 5174 | 99.8 | 967 | 8 | ADG39941 | Adg39941 Human myo |
| 9 | 5174 | 99.8 | 967 | 9 | ADY54944 | Ady54944 Chronic v |
| 10 | 5169 | 99.7 | 950 | 2 | AAY49501 | Aay49501 Human MET |

ALIGNMENTS

RESULT 1
ADG72483
ID    ADG72483 standard; protein; 949 AA.
XX
AC    ADG72483;
XX
DT    11-MAR-2004  (first entry)
XX
DE    Human aggrecanase (ADAMTS-1).

XX
KW    Human; aggrecanase; ADAMTS-1; rheumatoid arthritis; osteoarthritis;
KW    antiarthritic; osteopathic; enzyme.
XX
OS    Homo sapiens.
XX
PN    US6649377-B1.
XX
PD    18-NOV-2003.
XX
PF    09-MAY-2000; 2000US-00568559.
XX
PR    10-MAY-1999; 99US-0133343P.
XX
PA    (SYNT ) SYNTEX USA LLC.
XX
PI    Allard JD, Heller RA, Klonowski P, Vanwart HE;
XX
PT    New nucleic acid present in other than its natural environment, useful
PT    for preparing a composition for diagnosing or treating diseases
PT    associated with aggrecanase activity, e.g. rheumatoid arthritis or
PT    osteoarthritis.
XX
PS    Disclosure; SEQ ID NO 2; 26pp; English.
XX
CC    The present invention relates to the isolation of human aggrecanase
CC    (ADAMTS-1), and the polynucleotide sequence encoding it. Also disclosed
CC    are is a method of producing aggrecanase in vitro. The polynucleotide
CC    sequence encoding aggrecanase is useful for preparing a composition for
CC    diagnosing or treating diseases associated with aggrecanase activity e.g.
CC    rheumatoid arthritis or osteoarthritis. The present sequence represents
CC    human aggrecanase.
XX
DR    WPI; 2003-896162/82.
DR    N-PSDB; ADG72482.
XX
SQ    Sequence 949 AA;

Query Match             100.0%;  Score 5183;  DB 7;  Length 949;
Best Local Similarity   100.0%;
Matches  949; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy          1 GNAERAPGSRSFGPVPTLLLLLLAAALLAVSDALGRPSEEDEELLVVPELERAPGHGTTRLRL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GNAERAPGSRSFGPVPTLLLLLLAAALLAVSDALGRPSEEDEELLVVPELERAPGHGTTRLRL 60

Qy         61 HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSGTVNGDPSSAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSGTVNGDPSSAAA 120

Qy        121 LSLCEGVRGAPYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LSLCEGVRGAPYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180

Qy        181 GVVDDEPRPTGKAETTEDEDEGTEGEDEGAQWSPQDPALQGVGQPPGTGSIRKKRFVSSHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVVDDEPRPTGKAETTEDEDEGTEGEDEGAQWSPQDPALQGVGQPPGTGSIRKKRFVSSHR 240

Qy        241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300

Qy        301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360

Qy        361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420

Qy        421 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH 480

```
OM protein - protein search, using sw model

                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:             March 17, 2006, 17:58:35 ; Search time 49 Seconds
                                              (without alignments)
                                              1601.209 Million cell updates/sec

Title:              US-10-667-281-2
Perfect score:      5183
Sequence:           1 GNAERAPGSRSFPGPVPTLLL..........CDPLKPKHFIDFCTMABCS 949

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:    572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 10 summaries

Database :       Issued Patents AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5183 | 100.0 | 949 | 2 | US-09-568-559-2 | Sequence 2, Appli |
| 2 | 5169 | 99.7 | 967 | 2 | US-09-130-491-2 | Sequence 2, Appli |
| 3 | 4287.5 | 82.7 | 950 | 2 | US-09-321-987B-4 | Sequence 4, Appli |
| 4 | 3940 | 76.0 | 727 | 2 | US-09-445-023A-12 | Sequence 1, Appli |
| 5 | 3674 | 70.9 | 727 | 2 | US-09-445-023A-12 | Sequence 12, Appl |
| 6 | 3315 | 64.0 | 608 | 2 | US-09-130-491-13 | Sequence 13, Appl |
| 7 | 2812 | 54.3 | 551 | 2 | US-09-130-491-16 | Sequence 16, Appl |
| 8 | 2480.5 | 47.9 | 950 | 2 | US-10-009-332-1 | Sequence 1, Appli |
| 9 | 2332 | 45.0 | 887 | 2 | US-09-949-002-534 | Sequence 534, App |
| 10 | 2331.5 | 45.0 | 890 | 2 | US-09-949-002-394 | Sequence 394, App |

ALIGNMENTS

```
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-09-568-559-2

Query Match   100.0%;  Score 5183;  DB 2;  Length 949;
Best Local Similarity  100.0%;  Pred. No. 0;  Indels 0;  Gaps 0;
Matches 949;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GNAERAPGSRSFPGPVPTLLLLLLAAAALLAVSDALGRPSEEDEBELVVPELERAPGHGTTRLRL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GNAERAPGSRSFPGPVPTLLLLLLAAAALLAVSDALGRPSEEDEBELVVPELERAPGHGTTRLRL 60

Qy    61 HAFPDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLAHCFYSGTVNGDPSSAAA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 HAFPDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLAHCFYSGTVNGDPSSAAA 120

Qy   121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180

Qy   181 GVVDDEPRPTGKAETEDEDECTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GVVDDEPRPTGKAETEDEDECTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 240

Qy   241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300

Qy   301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360

Qy   361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420

Qy   421 HSQPWSPCSAYMITSFLDNGHGBCLMDKPQNPIQLPGDLPGTSYDANRQCQFTPGEDSKH 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 HSQPWSPCSAYMITSFLDNGHGBCLMDKPQNPIQLPGDLPGTSYDANRQCQFTPGEDSKH 480

Qy   481 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKHPDTPF 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKHPDTPF 540

Qy   541 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 600

Qy   601 KTFREEQCEAHNEFSKASFGGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFVLQPKVV 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 KTFREEQCEAHNEFSKASFGGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFVLQPKVV 660

Qy   661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKPFDKGCVCGNGNGSTCKKIISGSVTSAKPGY 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKPFDKGCVCGNGNGSTCKKIISGSVTSAKPGY 720

Qy   721 HDIIITPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 HDIIITPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV 780

Qy   781 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKBSFNAIPTSAW 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKBSFNAIPTSAW 840

Qy   841 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS 900
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:     March 17, 2006, 17:54:29 ; Search time 48 Seconds
            (without alignments)
            1902.286 Million cell updates/sec

Title:          US-10-667-281-2
Perfect score:  5183
Sequence:       1 GNAERAPGSRSRFGPVPTLLL..........CDPLKKPKHFIDFCTMAECS 949

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 10 summaries

Database :  PIR 80:*
            1:  pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 4291.5 | 82.8 | 951 | 2 | T00017 | gene ADAMTS-1 prot |
| 2 | 3074 | 59.3 | 550 | 2 | T47158 | hypothetical prote |
| 3 | 2136 | 41.2 | 837 | 2 | T00355 | hypothetical prote |
| 4 | 1613 | 31.1 | 2165 | 2 | T21371 | hypothetical prote |
| 5 | 1118 | 21.6 | 1205 | 2 | T18517 | procollagen N-endo |
| 6 | 647 | 12.5 | 1558 | 2 | C89114 | protein C37C3.6a [ |
| 7 | 647 | 12.5 | 2167 | 2 | T34395 | hypothetical prote |
| 8 | 634.5 | 12.2 | 1444 | 2 | T34956 | angiogenesis inhib |
| 9 | 475 | 9.2 | 860 | 2 | T16892 | hypothetical prote |
| 10 | 424.5 | 8.2 | 1059 | 2 | T22545 | hypothetical prote |

ALIGNMENTS

RESULT 1
T00017
gene ADAMTS-1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004
C;Accession: T00017
R;Kuno, K.; Iizasa, H.; Ohno, S.; Matsushima, K.
Genomics 46, 466-471, 1997
A;Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene
A;Reference number: Z14405; MUID:9811O583; PMID:9441751
A;Accession: T00017
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-951 <KUN>
A;Cross-references: UNIPARC:UPI000049F23; EMBL:AB001735; NID:g2809056; PIDN:BAA24501.
A;Experimental source: strain 129SVJ
C;Genetics:
A;Gene: ADAMTS-1
A;Genetics:
A;Gene: ADAMTS-1
A;Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
F;542-598/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match       82.8%;  Score 4291.5;  DB 2;  Length 951;
Best Local Similarity  82.3%;  Pred. No. 3.5e-286;
Matches 788;  Conservative 55;  Mismatches 99;  Indels 15;  Gaps 5;

```
Qy    1 GNAERAPGSRSRFGPVPTLLLLAAA---LLAVSDALGRPSEBEDEELVVPELERAPGHG--T 55
          | :||  || |::  ||||||:    |||  ||| ||||||:  :||:||:|||||  :
Db    2 GDVQRAARSRGSLSAHMLLLLASITMLLCARGAHGRPTEEDEELVLPSLERAPGHDSTT 61

Qy   56 TRLRLHAFDQQLDLRLRDDSSFLAPGFTLNQNVGRKSGSETPL--PETDLAHCFYSGTVNG 113
         |||||.||.||| |:|: ||:|||||||   ||| .|||   |  | .|||||||||||||
Db   62 TRLRLDAFCQQLHLKLQPDSGFLAPGFTLQTVGRSPGSEAQHLDPTGDLAHCFYSGTVNG 121

Qy  114 DPSSAAALSLCEGVRGAFYILGEAYFIQPLP-AASERLATAAPGEKPPAPLQFHLLRRNR 172
         ||.|||||||||||||||:||  :.|||| | .|.|||| |.| |  .|:|||||:||.|
Db  122 DPGSAAALSLCEGVRGAFYLLQGEBFFIQPAPGVATERLAPAVPEEBSSARPQFHILRRR 181

Qy  173 QGDVGGTCGVVDDEPRPTGKAETEDEDEGTEGBEDBGAQWSPQDPALQGVGQPTGTGSIRK 232
         :|. | .||| ||| |||      : .|::|:   ||    |       |    ||.|||
Db  182 RGSGGAKCGVMDDETLPT------SDSRPBSQNTRNQWPVRDPTPQDAGKPSGPGCSIRK 234

Qy  233 KRFVSSHRYVETMLVADQSMAEFHGSGLKHYLTLFRSVAARLYKHPSIRNSVSLVVVKIL 292
         ||||||.|||||||||||||| |||||||||||||.||||:|||||||||:.|||||||
Db  235 KRFVSSPRYVETMLVADQSMADFHGSGLKHYLTLFSVAARFYKHPSIRNSISLVVVKIL 294

Qy  293 VIHDEQKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTL 352
         ||:.||||||||||||||||||||||||||.|||||.|||||||||||||||||:|||||
Db  295 VIYBEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTAILFTRQDLCGSHTCDTL 354

Qy  353 GMADVGTVCDPSRSCSVIEDDGLQOAAFTTAHELGHVFNMPHDDAKQCASLNGVWQDSHMM 412
         ||||||||||||||||||||||||||||||||||||||||||||||.|||||||.|||:|
Db  355 GMADVGTVCDPSRSCSVIEDDGLQOAAFTTAHELGHVFNMPHDDAKGHCASLNGVTGDSHLM 414

Qy  413 ASMLSNLDHSQPWSPCSAYMITSFLDNGHGEBCLMDKPONPIQLPGDLPGTSYDANRQCQF 472
         ||||| ||||||||||||||:||||||||||||||||||||:|||.||||:|||||||||
Db  415 ASMLSSLDHSQPWSPCSAYMVTSFLDNGHGEBCLMDKPQNPIKLPSDLPGTLYDANRQCQF 474

Qy  473 TFGEDSKHCPDAASTCSTLWCTGTSGGVLAVCQTKHFPWADGTSCGEBGKRWCINGKCVNKTH 532
         ||||.|||||||||||.|||||||||||:|||||||||||||||||||||.||:.|||||| 
Db  475 TFGEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEBGKWCVSGKCVNKTD 534

Qy  533 RKHFDTPFHGSWMGWMGPWGDCSRTCGGGVQYTMRBCDNPVPKNGGKYCEGKRVYRSCNL 592
         .|||.||.||||..|.|||||||||||||||||||.|||||||||||||||||||||||:
Db  535 MKHFATPVHGSWGPWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVYRSCNI 594

Qy  593 EDCPDNNGKTFREEQCEBAHNEESKASGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYF 652
         ||||||||||||.|||.|||||:||||.|.   ||.||||||||||||||.|.|||||||
Db  595 EDCPDNNGKTFRRBQCERAHNEFSKASFGNEBPTVEWTPKYAGVSPKDRCKLTCRAKGIGYF 654

Qy  653 FVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGS 712
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db  655 FVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKMSGI 714

Qy  713 VTSAKPGYHDIIIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQ 772
         |||:.||||||:.||.||||||.:|||||||||||||||.||||||||||::|||||||
Db  715 VTSTRPGYHDIVTIPAGATNIEVTHRNQRGSRNNGSFLAIRAADGTYILNGNFTLSTLEQ 774

Qy  773 DIMYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKCESFN 832
         |:.||||||||||||||||||||||||||.||||||..|.||||||:|||..|||.||.|
Db  775 DLTYKGTVLRYSGSSAALERIRSFSPLKBPLTIQVLMYGHALRPKIKFTYFMKKKTESPN 834

Qy  833 AIPTFSAWVIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCP 892
         ||||||.|||||||||||:|| ||||||.||||||.||||||||||||||||||||.|||
Db  835 AIPTFSEWVIEEWGECSKTCGSGWQRRVVQCRDINGHPASECAKEVKPASTRPCADLPCP 894

Qy  893 QWQLGEWSSCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS 949
         ||:||||:|||:||.||.|||.|.|||||  .:.||.||.||:||||||||||.:||
Db  893 ...
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:    March 17, 2006, 17:51:04 ; Search time 242 Seconds
(without alignments)
2766.721 Million cell updates/sec

Title:
Perfect score:    5183
Sequence:    1 GNAERAPGSRSFGPVPTLLLL..........CDPLKKPKHFIDFCTMAECS 949

Scoring table:    BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched:    2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :    UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5169 | 99.7 | 967 | 1 | Q9UHI8 | ATS1_HUMAN Q9uhi8 homo sapien |
| 2 | 5164 | 99.6 | 967 | 2 | Q5HYL0 | Q5hyl0 homo sapien |
| 3 | 5161 | 99.6 | 967 | 2 | Q8N826 | Q8n826 homo sapiens |
| 4 | 4750 | 91.6 | 967 | 2 | Q56D5 | Q56d5 pongo pygma |
| 5 | 4291.5 | 82.8 | 911 | 2 | Q56D5 | Q56d5 pongo pygma |
| 6 | 4285 | 82.7 | 968 | 1 | ATS1_MOUSE | P97857 mus musculu |
| 7 | 4279 | 82.6 | 967 | 2 | Q68EJ2 | Q68ej2 rattus norv |
| 8 | 3921.5 | 75.7 | 759 | 1 | ATS1_RAT | Q9wuq1 rattus norv |
| 9 | 3718 | 71.7 | 928 | 2 | Q8HZM8 | Q8hzm8 equus cabal |
| 10 | 2512.5 | 48.5 | 950 | 2 | Q5U261_XENLA | Q5u261 xenopus lae |
|  |  |  |  | 2 | Q504Z2_MOUSE | Q504z2 mus musculu |

ALIGNMENTS

RESULT 1
ATS1_HUMAN

ID    ATS1_HUMAN    STANDARD;    PRT;    967 AA.
AC    Q9UHI8; Q9NSJ8; Q9P2K0; Q9UH83; Q9UP80;
DT    30-MAY-2000 (Rel. 39, Created)
DT    16-OCT-2001 (Rel. 40, Last sequence update)
DT    13-SEP-2005 (Rel. 48, Last annotation update)
DE    ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE    with thrombospondin motifs 1) (ADAM-TS 1) (ADAMTS1) (METH-1).
GN    Name=ADAMTS1; Synonyms=KIAA1346, METH1;
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC    Homo.
OX    NCBI_TaxID=9606;
RN    [1]

RP    NUCLEOTIDE SEQUENCE.
RA    Casas C., Pritchard M.A., Estivill X., Arbones M.L.;
RT    "Cloning, characterization and mapping on human chromosome 21 of the
RT    orthologue of murine Adamts-1.";
RL    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN    [2]
RP    NUCLEOTIDE SEQUENCE, AND FUNCTION.
RC    TISSUE=Heart;
RX    MEDLINE=99367466; PubMed=10438512; DOI=10.1074/jbc.274.33.23349;
RA    Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
RA    Lombardo M., Iruela-Arispe M.L.;
RT    "METH-1, a human ortholog of ADAMTS-1, and METH-2 are members of a new
RT    family of proteins with angio-inhibitory activity.";
RL    J. Biol. Chem. 274:23349-23357(1999).
RN    [3]
RP    NUCLEOTIDE SEQUENCE.
RC    TISSUE=Endothelial cell;
RX    MEDLINE=20247184; PubMed=10785405;
RA    Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,
RA    Rosenthal A., Thierauch K.H.;
RT    "Differential gene expression by endothelial cells in distinct
RT    angiogenic states.";
RL    Eur. J. Biochem. 267:2820-2830(2000).
RN    [4]
RP    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC    TISSUE=Brain;
RX    MEDLINE=20181126; PubMed=10718198;
RA    Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
RT    "Prediction of the coding sequences of unidentified human genes. XVI.
RT    The complete sequences of 150 new cDNA clones from brain which code
RT    for large proteins in vitro.";
RL    DNA Res. 7:65-73(2000).
RN    [5]
RP    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX    MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA    Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA    Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K, Groner Y.,
RA    Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA    Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA    Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA    Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA    Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA    Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA    Scharfe M., Schoen O., Desario A., Reichel J., Kauer G., Bloecker H.,
RA    Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA    Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA    Lehrach H., Reinhardt R., Yaspo M.-L.;
RT    "The DNA sequence of human chromosome 21.";
RL    Nature 405:311-319(2000).
RN    [6]
RP    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 418-967.
RC    TISSUE=Melanoma;
RG    The German cDNA consortium;
RL    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC    -!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
CC        involved in its turnover (By similarity). Has angiogenic inhibitor
CC        activity. Active metalloprotease, which may be associated with
CC        various inflammatory processes as well as development of cancer
CC        cachexia. May play a critical role in follicular rupture.
CC    -!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1938-Glu-|-Leu-1939
CC        site, within the chondroitin sulfate attachment domain.
CC    -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC    -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC        matrix (By similarity).
CC    -!- DOMAIN: The spacer domain and the TSP type-1 domains are important
CC        for a tight interaction with the extracellular matrix.
CC    -!- PTM: The precursor is cleaved by a furin endopeptidase (By
CC        similarity).
CC    -!- SIMILARITY: Contains 1 disintegrin domain.
CC    -!- SIMILARITY: Contains 1 peptidase M12B domain.
CC    -!- SIMILARITY: Contains 3 TSP type-1 domains.
CC    ------------------------------------------------------------------------
CC    This Swiss-Prot entry is copyright. It is produced through a collaboration

```
OM protein - protein search, using sw model

                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:             March 17, 2006, 18:10:45 ; Search time 25 Seconds
                                            (without alignments)
                                            1086.525 Million cell updates/sec

Title:              US-10-667-281-2
Perfect score:      5183
Sequence:           1 GNARRAPGSRSFGPVPTLLL..........CDPLKKPKHFIDFCTMAECS 949

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters:      169630

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 10 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :          Published Applications_AA_New:*
                    1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                    2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                    3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                    4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                    5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                    6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                    7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                    8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

Result              %       Query
No.     Score   Match   Length  DB  ID                  Description
----    -----   -----   ------  --  --                  -----------
1       5174    99.8    967     6   US-10-995-561-979   Sequence 979, App
2       5174    99.8    967     6   US-10-995-561-980   Sequence 980, App
3       5174    99.8    967     6   US-10-821-234-1251  Sequence 1251, Ap
4       5169    99.7    999     7   US-11-169-041-191   Sequence 191, App
5       2334.5  45.0    890     7   US-11-106-623-28    Sequence 28, Appl
6       2136    41.2    837     7   US-11-127-877-74    Sequence 74, Appl
7       1774    34.2    1076    7   US-11-109-157A-5    Sequence 5, Appl
8       1734    33.5    1907    7   US-11-039-398-25    Sequence 25, Appl
9       1622.5  31.3    785     7   US-11-109-157A-6    Sequence 6, Appl
10      1331    25.7    1686    7   US-11-109-157A-1    Sequence 1, Appli

                                ALIGNMENTS
```

```
Query Match 94.8%;  Best Local Similarity 99.8%;
Matches 948;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1   GNARRAPGSRSFGPVPTLLLLLLLAAALLLAVSDALGRPSEEDEELVVPELERAPGHGTTRLRL 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   GNARRAPGSRSFGPVPTLLLLLLLAAALLLAVSDALGRPSEEDEELVVPELERAPGHGTTRLRL 60

Qy      61  HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLIAHCFYSGTVNGDPSSAAA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79  HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLIAHCFYSGTVNGDPSSAAA 138

Qy      121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAPAPGEKPPAPLQFHLLRRNRQGDVGGTC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      139 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAPAPGEKPPAPLQFHLLRRNRQGDVGGTC 198

Qy      181 GVVDDEPRPTGKAETEDEDEGTEGEDEGAGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      199 GVVDDEPRPTGKAETEDEDEGTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 258

Qy      241 YVETMLVADQSMAEFHGSGLKHYLLTFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      259 YVETMLVADQSMAEFHGSGLKHYLLTFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 318

Qy      301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      319 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 378

Qy      361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      379 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 438

Qy      421 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      439 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH 498

Qy      481 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKIFDTPF 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      499 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTDRKIFDTPF 558

Qy      541 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      559 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 618

Qy      601 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFVLQPKVV 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      619 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFVLQPKVV 678

Qy      661 DGTPCSPDSTSVCVQGQCVKAGCDRIIIDSKKKFDKCGVCGGNGSTCKKISGSVSAKPGY 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      679 DGTPCSPDSTSVCVQGQCVKAGCDRIIIDSKKKFDKCGVCGGNGSTCKKISGSVSAKPGY 738

Qy      721 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      739 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV 798

Qy      781 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      799 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW 858

Qy      841 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      859 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS 918
```

OM protein - protein search, using sw model

```
                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:           March 17, 2006, 18:09:50 ; Search time 169 Seconds
                  (without alignments)
                  2346.272 Million cell updates/sec

Title:            US-10-667-281-2
Perfect score:    5183
Sequence:         1 GNAERAPGSRSFGPVPTLLLL.........CDPLKPKHFIDFCTMAECS 949

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:   1867569

Post-processing:  Minimum Match 0%
Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Database :        Published_Applications_AA_Main:*
                  1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                  2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                  3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                  Listing first 10 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5183 | 100.0 | 949 | 5 | US-10-667-281-2 | Sequence 2, Appli |
| 2 | 5174 | 99.8 | 950 | 5 | US-10-741-600-1605 | Sequence 1605, Ap |
| 3 | 5174 | 99.8 | 950 | 5 | US-10-973-858-14 | Sequence 14, Appl |
| 4 | 5174 | 99.8 | 967 | 5 | US-10-741-600-1603 | Sequence 1603, Ap |
| 5 | 5174 | 99.8 | 967 | 5 | US-10-741-600-1604 | Sequence 1604, Ap |
| 6 | 5174 | 99.8 | 967 | 5 | US-10-923-035-37 | Sequence 37, Appl |
| 7 | 5174 | 99.8 | 967 | 5 | US-10-756-149-5619 | Sequence 5619, Ap |
| 8 | 5169 | 99.7 | 950 | 3 | US-09-373-658-2 | Sequence 2, Appli |
| 9 | 5169 | 99.7 | 950 | 3 | US-09-989-687-2 | Sequence 2, Appli |
| 10 | 5169 | 99.7 | 967 | 4 | US-10-105-929-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-10-667-281-2
; Sequence 2, Application US/10667281
; Publication No. US2005010091 6A1
; GENERAL INFORMATION:
;  APPLICANT: Klonowski, Paul
;  APPLICANT: Allard, John
;  APPLICANT: Heller, Renu
;  APPLICANT: Van Wart, Harold
;  TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
;  TITLE OF INVENTION: Compositions Encoding the Same
;  FILE REFERENCE: ROCH-002

```
; CURRENT APPLICATION NUMBER: US/10/667,281
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 949
;   TYPE: PRT
;   ORGANISM: human
; US-10-667-281-2

Query Match             100.0%;  Score 5183;  DB 5;  Length 949;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  949;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy      1 GNAERAPGSRSFGPVPTLLLLAAALLAVSDALGRPSEEDEELVVPELERAPGHGTTRLRL 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GNAERAPGSRSFGPVPTLLLLAAALLAVSDALGRPSEEDEELVVPELERAPGHGTTRLRL 60

Qy     61 HAPDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLAHCFYSGTVNGDPSSAAA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 HAPDQQLDLELRPDSSFLAPGFTLQNVGRKSGSSETPLPETDLAHCFYSGTVNGDPSSAAA 120

Qy    121 LSLCEGVRGAFYLLGBAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LSLCEGVRGAFYLLGBAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC 180

Qy    181 GVVDDEPRPTGKAETEDEDEGTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVVDDEPRPTGKAETEDEDEGTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSHR 240

Qy    241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVVKILVIHDEQKG 300

Qy    301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGTV 360

Qy    361 CDPSRSCSVIEDDGLQOAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CDPSRSCSVIEDDGLQOAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD 420

Qy    421 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTGEDSKH 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 HSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTGEDSKH 480

Qy    481 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKHFDTPF 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKHFDTPF 540

Qy    541 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG 600

Qy    601 KTFRBEQCEAHNEFSKASPGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFPVLQPKVV 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 KTFRBEQCEAHNEFSKASPGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFPVLQPKVV 660

Qy    661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAKPGY 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAKPGY 720

Qy    721 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLBQDIMYKGVV 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLBQDIMYKGVV 780

Qy    781 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 LRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW 840
```